

Amendments to the Specification:

Please delete the Background of the Invention title and the paragraph following, namely, paragraph [0002] and replace therefore:

-- CROSS-REFERENCE TO RELATED APPLICATIONS

[0002] This application is a continuation-in-part and claims priority based on United States Patent Application, 10/272,509, filed October 16, 2002, which is a continuation-in-part of United States Patent Application, 09/425,798, filed October 25, 1999, now U.S. Patent No. 6,423,493, which is a continuation-in-part of United States Patent application, 09/425,804, filed October 25, 1999, which is a continuation-in-part of claims priority to U.S. Provisional Application Serial No. 60/105,600, filed October 26, 1998.

STATEMENT OF FEDERALLY FUNDED RESEARCH

[0003] This work was supported by the following United States grants: NIH AI27744 – Combinatorial and rational design of aptamers targeting HIV, NHLBI N01-HV-28184 – Proteomic Technologies to Study Airway Inflammation; and NIAID U01 AI054827 – Biodefense Proteomics Collaboratory; the government may own certain rights.

BACKGROUND OF THE INVENTION

[0004] Without limiting the scope of the invention, its background is described in connection with oligonucleotide agents and with methods for the isolation of modified oligonucleotides that bind specifically to target proteins. --

Please amend paragraph 90 as follows:

[0090] Analysis of Thioaptamer Sequences. The DNA sequences were obtained from various rounds of selection (5, 9, 12, and 18 round) and aligned using, e.g., the ClustalW algorithm (version 1.8), which is available from, e.g., a bioinformatics web site at Baylor College of Medicine (<http://searchlauncher.bme.tmc.edu>). Secondary structure prediction of single-stranded DNA was conducted using, e.g., the *mfold* program (Zuker, et al., 2003), available at <http://www.bioinfo.rpi.edu/applications/mfold/old/dna/form1.cgi>.